1600

RAW SEQUENCE LISTING   DATE: 06/05/2003
PATENT APPLICATION: US/09/068,507B   TIME: 13:44:51

#34

    Input Set : A:\2003-05-30 1380-0122P.ST25.txt
    Output Set: N:\CRF4\06052003\I068507B.raw

```
   3 <110> APPLICANT: EIJSINK, VINCENT et al.
   5 <120> TITLE OF INVENTION: EXPRESSION SYSTEM IN MICROORGANISM AND ITS USE FOR
EXPRESSING
   6       HETEROLOGOUS AND HOMOLOGOUS PROTEINS
   8 <130> FILE REFERENCE: 1380-0122P
  10 <140> CURRENT APPLICATION NUMBER: US 09/068,507B
C--> 11 <141> CURRENT FILING DATE: 1998-07-18
  13 <160> NUMBER OF SEQ ID NOS: 19
  15 <170> SOFTWARE: PatentIn version 3.1
  17 <210> SEQ ID NO: 1
  18 <211> LENGTH: 26
  19 <212> TYPE: PRT
  20 <213> ORGANISM: Lactobacillus plantarum
  22 <400> SEQUENCE: 1
  24 Lys Ser Ser Ala Tyr Ser Leu Gln Met Gly Ala Thr Ala Ile Lys Gln
  25 1               5                   10                  15
  28 Val Lys Lys Leu Phe Lys Lys Trp Gly Trp
  29             20                  25
  32 <210> SEQ ID NO: 2
  33 <211> LENGTH: 114
  34 <212> TYPE: DNA
  35 <213> ORGANISM: Lactobacillus sake
  37 <220> FEATURE:
  38 <221> NAME/KEY: CDS
  39 <222> LOCATION: (1)..(114)
  40 <223> OTHER INFORMATION:
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  43 atg atg ata ttt aaa aaa ctt tca gaa aaa gaa ttg caa aaa ata aac      48
  44 Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn
  45 1               5                   10                  15
  47 ggt ggt atg gca gga aat agt tct aat ttt att cat aag att aaa caa      96
  48 Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln
  49             20                  25                  30
  51 att ttt acc cat cgt taa                                             114
  52 Ile Phe Thr His Arg
  53          35
  56 <210> SEQ ID NO: 3
  57 <211> LENGTH: 37
  58 <212> TYPE: PRT
  59 <213> ORGANISM: Lactobacillus sake
  61 <400> SEQUENCE: 3
  63 Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn
  64 1               5                   10                  15
  67 Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln
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 68            20                25                30
 71 Ile Phe Thr His Arg
 72          35
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 186
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Lactobacillus sake
 80 <220> FEATURE:
 81 <221> NAME/KEY: CDS
 82 <222> LOCATION: (1)..(186)
 83 <223> OTHER INFORMATION:
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W--> **85 <400> 4**
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 86 atg gaa aag ttt att gaa tta tct tta aaa gaa gta aca gca att aca       48
 87 Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
 88 1               5                   10                  15
 90 ggt gga aaa tat tat ggt aac ggt gta cac tgt gga aaa cat tca tgt       96
 91 Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
 92            20                25                30
 94 acc gta gac tgg gga aca gct att gga aat atc gga aat aat gca gct      144
 95 Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
 96            35                40                45
 98 gca aac tgg gcc aca ggc gga aac gct ggc tgg aat aaa taa            186
 99 Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys
100        50                55                  60
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 61
105 <212> TYPE: PRT
106 <213> ORGANISM: Lactobacillus sake
108 <400> SEQUENCE: 5
110 Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr
111 1               5                   10                  15
114 Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys
115            20                25                30
118 Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala
119            35                40                45
122 Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys
123        50                55                  60
126 <210> SEQ ID NO: 6
127 <211> LENGTH: 81
128 <212> TYPE: DNA
129 <213> ORGANISM: Lactobacillus sake
131 <400> SEQUENCE: 6
132 gagttcttaa cgttaatccg aaaaaaacta acgttaatat taaaaaataa gatccgcttg       60
134 tgaattatgt ataatttgat t                                         81
137 <210> SEQ ID NO: 7
138 <211> LENGTH: 80
139 <212> TYPE: DNA
140 <213> ORGANISM: Lactobacillus sake
142 <400> SEQUENCE: 7
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Input Set : **A:\2003-05-30 1380-0122P.ST25.txt**
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143 cgcatattaa cgtttaaccg ataaagttga acgttaatat ttttttgcg cagaaatggt    60
145 aaattgaagc ataatagtct                                              80
148 <210> SEQ ID NO: 8
149 <211> LENGTH: 81
150 <212> TYPE: DNA
151 <213> ORGANISM: Lactobacillus sake
153 <400> SEQUENCE: 8
154 gcagcattaa cgttaatttt gataaacgta acgttaatgg ataatcatcc tgtttacaaa    60
156 tagtgtatga cataattaag t                                            81
159 <210> SEQ ID NO: 9
160 <211> LENGTH: 81
161 <212> TYPE: DNA
162 <213> ORGANISM: Lactobacillus sake
164 <400> SEQUENCE: 9
165 ttgatattag cgtttaacag ttaaattaat acgttaataa ttttttgtc tttaaatagg    60
167 gatttgaagc ataatggtgt t                                            81
170 <210> SEQ ID NO: 10
171 <211> LENGTH: 81
172 <212> TYPE: DNA
173 <213> ORGANISM: Lactobacillus plantarum
175 <400> SEQUENCE: 10
176 tggtgattca cgtttaaatt taaaaaatgt acgttaatag aaataattcc tccgtacttc    60
178 aaaaacacat tatcctaaaa g                                            81
181 <210> SEQ ID NO: 11
182 <211> LENGTH: 80
183 <212> TYPE: DNA
184 <213> ORGANISM: Staphylococcus aureus
186 <400> SEQUENCE: 11
187 tacatttaac agttaagtat ttatttccta cagttaggca atataatgat aaaagattgt    60
189 actaaatcgt ataatgacag                                              80
192 <210> SEQ ID NO: 12
193 <211> LENGTH: 80
194 <212> TYPE: DNA
195 <213> ORGANISM: Staphylococcus aureus
197 <400> SEQUENCE: 12
198 aaaaatttac agttaagaat aaaaaacgac tagttaagaa aaattggaaa aataaatgct    60
200 tttagcatgt ttaatataac                                              80
204 <210> SEQ ID NO: 13
205 <211> LENGTH: 7597
206 <212> TYPE: DNA
207 <213> ORGANISM: Lactobacillus sakei
210 <220> FEATURE:
211 <221> NAME/KEY: -35_signal
212 <222> LOCATION: (412)..(417)
214 <220> FEATURE:
215 <221> NAME/KEY: -10_signal
216 <222> LOCATION: (439)..(444)
218 <220> FEATURE:
219 <221> NAME/KEY: gene
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220 <222> LOCATION: (572)..(1918)
221 <223> OTHER INFORMATION: gene="sppK"
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (572)..(1918)
227 <220> FEATURE:
228 <221> NAME/KEY: CDS
229 <222> LOCATION: (1920)..(2666)
231 <220> FEATURE:
232 <221> NAME/KEY: gene
233 <222> LOCATION: (1920)..(2666)
234 <223> OTHER INFORMATION: gene="sppR"
236 <220> FEATURE:
237 <221> NAME/KEY: -35_signal
238 <222> LOCATION: (2712)..(2717)
240 <220> FEATURE:
241 <221> NAME/KEY: -10_signal
242 <222> LOCATION: (2736)..(2741)
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (2813)..(2998)
248 <220> FEATURE:
249 <221> NAME/KEY: gene
250 <222> LOCATION: (2813)..(2998)
251 <223> OTHER INFORMATION: gene="sppA"
253 <220> FEATURE:
254 <221> NAME/KEY: sig_peptide
255 <222> LOCATION: (2813)..(2866)
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (3092)..(3388)
261 <220> FEATURE:
262 <221> NAME/KEY: gene
263 <222> LOCATION: (3092)..(3388)
264 <223> OTHER INFORMATION: gene="spiA"
266 <220> FEATURE:
267 <221> NAME/KEY: -35_signal
268 <222> LOCATION: (3654)..(3659)
270 <220> FEATURE:
271 <221> NAME/KEY: -10_signal
272 <222> LOCATION: (3675)..(3680)
274 <220> FEATURE:
275 <221> NAME/KEY: CDS
276 <222> LOCATION: (3739)..(5895)
278 <220> FEATURE:
279 <221> NAME/KEY: gene
280 <222> LOCATION: (3739)..(5895)
281 <223> OTHER INFORMATION: gene="sppT"
283 <220> FEATURE:
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RAW SEQUENCE LISTING
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Input Set : A:\2003-05-30 1380-0122P.ST25.txt
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284 <221> NAME/KEY: CDS
285 <222> LOCATION: (5910)..(7286)
287 <220> FEATURE:
288 <221> NAME/KEY: gene
289 <222> LOCATION: (5910)..(7286)
290 <223> OTHER INFORMATION: gene="sppE"
292 <400> SEQUENCE: 13
·293 ccggctcttt gaccataagc acctaggtcg attaataatt gttcttcaga tttattgaga      60
295 tgaattttac caaagccaac actataaata taatttgcga ggcggttgac taacacttca     120
297 ggattcttgg cagtttcaag tgtgagatag acctgactca aaacatcggt aatgtcgaga     180
299 agcgcgtttg atttatctgg atgagccatt aggctgttgt aaagtgtatg aatgttttcc     240
301 ttagcaattt cttgattagt cataatgaaa agcctccaca aaaagtatta tcaacatctg     300
303 ttctagtctt cttagtaaat tttgtcaact tcaatagagt tcttaacgtt aatccgaaaa     360
305 aaactaacgt taatattaaa aaataagatc cgcttgtgaa ttatgtataa tttgattaga     420
307 ctaaagaata ggagaaagta tgatgatatt taaaaaactt tcagaaaaag aattgcaaaa     480
309 aataaacggt ggtatggcag gaaatagttc taattttatt cataagatta aacaaatttt     540
311 tacccatcgt taagataggt tgttggtgag c atg tta tat acg gat gta tcg     592
312                                    Met Leu Tyr Thr Asp Val Ser
313                                     1               5
315 gtt tcc tta atg caa aat ttt gtt gct atc tta tta att ttt cta tta     640
316 Val Ser Leu Met Gln Asn Phe Val Ala Ile Leu Leu Ile Phe Leu Leu
317         10                  15                  20
319 tat aga tat att caa aga aag ata aca ttt aaa cgg atc ata tta gat     688
320 Tyr Arg Tyr Ile Gln Arg Lys Ile Thr Phe Lys Arg Ile Ile Leu Asp
321     25                  30                  35
323 att tta ata gcg att att ttt tca ata tta tat ctg ttt att tca gat     736
324 Ile Leu Ile Ala Ile Ile Phe Ser Ile Leu Tyr Leu Phe Ile Ser Asp
325 40                  45                  50                  55
327 gcg tca tta ctt gta atg gta tta atg cga tta ggg tgg cat ttt cat     784
328 Ala Ser Leu Leu Val Met Val Leu Met Arg Leu Gly Trp His Phe His
329                 60                  65                  70
331 caa caa aaa gaa aat aag ata aaa acg act gat aca gct aat tta att     832
332 Gln Gln Lys Glu Asn Lys Ile Lys Thr Thr Asp Thr Ala Asn Leu Ile
333             75                  80                  85
335 cta att atc gtg atc cag tta ttg tta gtt gcg gtt ggg act att att     880
336 Leu Ile Ile Val Ile Gln Leu Leu Leu Val Ala Val Gly Thr Ile Ile
337         90                  95                  100
339 agt cag ttt acc ata tcg att atc aaa agt gat ttc agc caa aat ata     928
340 Ser Gln Phe Thr Ile Ser Ile Ile Lys Ser Asp Phe Ser Gln Asn Ile
341     105                 110                 115
343 ttg aac aat agt gca aca gat ata act tta tta ggt att ttc ttt gct     976
344 Leu Asn Asn Ser Ala Thr Asp Ile Thr Leu Leu Gly Ile Phe Phe Ala
345 120                 125                 130                 135
347 gtt tta ttt gac ggc ttg ttc ttt ata tta ttg aag aat aag cgg act    1024
348 Val Leu Phe Asp Gly Leu Phe Phe Ile Leu Leu Lys Asn Lys Arg Thr
349             140                 145                 150
351 gaa tta caa cat tta aat caa gaa atc att gaa ttt tcg tta gaa aaa    1072
352 Glu Leu Gln His Leu Asn Gln Glu Ile Ile Glu Phe Ser Leu Glu Lys
353             155                 160                 165
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VERIFICATION SUMMARY   DATE: 06/05/2003
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```
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:40
L:85 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:83
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